

FILE 'MEDLINE, EMBASE, USPATFULL, BIOSIS, CAPLUS' ENTERED AT 15:20:12 ON  
24 JAN 2005

L1	1510 S (BMP RECEPTOR)
L2	4 S L1 AND PY<1994
L3	3 S (CFK1-23A)
L4	81 S L1 AND (WOZNEY OR CELESTE OR THIES OR YAMAJI)
L5	85 S L2 OR L3 OR L4
L6	82 DUP REM L5 (3 DUPLICATES REMOVED)

Title: US-10-600-645-1  
 Perfect score: 1813  
 Sequence: 1 CTAGTGGATCCCCCGGGCTG.....TTCAGGACTCTGCAGAATGC 1813

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : GenEmbl:\*  
 1: gb\_ba:\*  
 2: gb\_htg:\*  
 3: gb\_in:\*  
 4: gb\_om:\*  
 5: gb\_ov:\*  
 6: gb\_pat:\*  
 7: gb\_ph:\*  
 8: gb\_pl:\*  
 9: gb\_pr:\*  
 10: gb\_ro:\*  
 11: gb\_sts:\*  
 12: gb\_sy:\*  
 13: gb\_un:\*  
 14: gb\_vi:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	%		Query		DB	ID	Description
	Score	Match	Length				
1	1813	100.0	1813	6	AR169902	AR169902 Sequence	
2	1813	100.0	1813	6	AR382508	AR382508 Sequence	
3	1750.4	96.5	3003	10	RATRALK3	D38082 Rat mRNA fo	
4	1750.4	96.5	3167	10	S75359	S75359 bone morpho	
5	1595.8	88.0	1599	10	RATRB4R1	D17667 Rat mRNA fo	
6	1584.6	87.4	2292	10	MUSBMPRC	D16250 Mus musculu	
7	1584.6	87.4	5288	10	BC042611	BC042611 Mus muscu	
8	1581.4	87.2	2070	6	A38817	A38817 Sequence 13	
9	1581.4	87.2	2070	6	AR140650	AR140650 Sequence	
10	1581.4	87.2	2070	6	AR164274	AR164274 Sequence	
11	1581.4	87.2	2070	6	AR264352	AR264352 Sequence	
12	1581.4	87.2	2070	6	AR475173	AR475173 Sequence	
13	1574.2	86.8	2402	6	AR144415	AR144415 Sequence	
14	1574.2	86.8	2402	6	AR174013	AR174013 Sequence	

	15	1574.2	86.8	2402	6	BD191976	BD191976 The use o
	16	1574.2	86.8	2402	10	MMU04672	U04672 Mus musculu
	17	1488.6	82.1	1599	10	AY365062	AY365062 Mus muscu
	18	1488.6	82.1	1599	10	MMALK3A	Z23154 M.musculus
	19	1424.4	78.6	2056	10	MMU04673	U04673 Mus musculu
	20	1387	76.5	2932	6	A38809	A38809 Sequence 5
	21	1387	76.5	2932	6	AR140646	AR140646 Sequence
	22	1387	76.5	2932	6	AR164270	AR164270 Sequence
	23	1387	76.5	2932	6	AR264348	AR264348 Sequence
	24	1387	76.5	2932	6	AR408534	AR408534 Sequence
	25	1387	76.5	2932	6	AR475169	AR475169 Sequence
	26	1387	76.5	2932	9	HSALK3A	Z22535 H.sapiens A
	27	1385.4	76.4	3625	9	BC028383	BC028383 Homo sapi
	28	1374.4	75.8	2892	6	CQ720881	CQ720881 Sequence
	29	1355.8	74.8	2861	6	CQ718018	CQ718018 Sequence
c	30	1355.8	74.8	93893	9	AL669984	AL669984 Human DNA
	31	1065.6	58.8	1969	5	CHKBRK1R	L49204 Gallus gall
	32	1032.4	56.9	1602	5	AF189777	AF189777 Coturnix
c	33	923.8	51.0	178089	2	AC010929	AC010929 Homo sapi
c	34	923.8	51.0	179604	9	AP002959	AP002959 Homo sapi
c	35	892	49.2	239655	2	AC096969	AC096969 Rattus no
	36	850.2	46.9	2333	5	BC070551	BC070551 Xenopus l
	37	850.2	46.9	2395	5	D32066	D32066 Xenopus lae
	38	847	46.7	2315	5	XLU16654	U16654 Xenopus lae
	39	846.2	46.7	2206	5	D32067	D32067 Xenopus lae
	40	846.2	46.7	2240	5	BC071081	BC071081 Xenopus l
	41	833.4	46.0	1281	6	CQ734017	CQ734017 Sequence
	42	781.2	43.1	2494	5	AB011826	AB011826 Danio rer
	43	716	39.5	1944	10	MMALK6A	Z23143 M.musculus
	44	716	39.5	1952	6	A38821	A38821 Sequence 17
	45	716	39.5	1952	6	AR140652	AR140652 Sequence

Title: US-10-600-645-1  
 Perfect score: 1813  
 Sequence: 1 CTAGTGGATCCCCCGGGCTG.....TTCAGGACTCTGCAGAATGC 1813

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : N\_Geneseq\_23Sep04:\*  
 1: geneseqn1980s:\*  
 2: geneseqn1990s:\*  
 3: geneseqn2000s:\*  
 4: geneseqn2001as:\*  
 5: geneseqn2001bs:\*  
 6: geneseqn2002as:\*  
 7: geneseqn2002bs:\*  
 8: geneseqn2003as:\*  
 9: geneseqn2003bs:\*  
 10: geneseqn2003cs:\*  
 11: geneseqn2003ds:\*  
 12: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

		%						
Result	Query							
No.	Score	Match	Length	DB	ID	Description		
1	1813	100.0	1813	2	AAQ83530	Aaq83530	Sequence	
2	1581.4	87.2	2070	2	AAZ09847	Aaz09847	Human mAL	
3	1579.8	87.1	2070	2	AAQ66640	Aaq66640	Mouse Act	
4	1574.2	86.8	2402	2	AAQ90184	Aaq90184	BRK-1 DNA	
5	1574.2	86.8	2402	2	AAT27228	Aat27228	Bone morp	
6	1574.2	86.8	2402	2	AAT28021	Aat28021	Mouse BMP	
7	1574.2	86.8	2402	2	AAV71972	Aav71972	Mouse BMP	
8	1424.4	78.6	2056	2	AAQ90183	Aaq90183	Truncated	
9	1387	76.5	2932	2	AAT06031	Aat06031	Human ALK	
10	1387	76.5	2932	2	AAZ09843	Aaz09843	Human hAL	
11	1387	76.5	2932	5	AAS87057	Aas87057	DNA encod	
12	1387	76.5	2932	10	ACF05952	Acf05952	Human bon	
13	1385.4	76.4	2932	2	AAQ66636	Aaq66636	Human Act	
14	1374.6	75.8	2623	8	AAD53821	Aad53821	DNA used	
15	1258.8	69.4	2730	5	AAS87064	Aas87064	DNA encod	
16	1104	60.9	1743	10	ADE07106	Ade07106	Novel cod	

17	978.2	54.0	1185	12	ACH87174	Ach87174 Human gen
18	918	50.6	1929	10	ADE07107	Ade07107 Novel cod
19	810.4	44.7	1695	5	AAS87063	Aas87063 DNA encod
20	773.8	42.7	2659	10	ADC74824	Adc74824 Human pro
21	716	39.5	1952	2	AAT06032	Aat06032 Mouse ALK
22	716	39.5	1952	2	AAZ09849	Aaz09849 Human mAL
23	714.4	39.4	1952	2	AAQ66642	Aaq66642 Mouse Act
24	707.6	39.0	1575	8	ACD13394	Acd13394 Human DNA
25	707.6	39.0	2032	6	ABK92206	Abk92206 Prostate
26	707.6	39.0	2032	6	ABT07695	Abt07695 Breast ca
27	707.6	39.0	2032	6	ABK90314	Abk90314 DNA encod
28	707.6	39.0	2032	8	ABT17075	Abt17075 Androgen-
29	707.6	39.0	2032	10	ACF05953	Acf05953 Human bon
30	707.6	39.0	2032	10	ADB80499	Adb80499 Ovarian c
31	707.6	39.0	2032	10	AAD63426	Aad63426 Human bon
32	707.6	39.0	2032	11	ADN38749	Adn38749 Cancer/an
33	707.6	39.0	2032	11	ADN39562	Adn39562 Cancer/an
34	707.6	39.0	2032	11	ADN39518	Adn39518 Cancer/an
35	707.6	39.0	2032	11	ADN39470	Adn39470 Cancer/an
36	707.6	39.0	2424	5	ABV28912	Abv28912 Human pro
37	707.6	39.0	2424	5	ABV23076	Abv23076 Human pro
38	707.6	39.0	3722	8	ACC49548	Acc49548 Tumour-as
39	707.6	39.0	4524	8	ACC72065	Acc72065 Bcu224 ge
40	700	38.6	1612	5	AAD11871	Aad11871 Wild-type
41	698.4	38.5	1612	5	AAD11872	Aad11872 Booroola
42	697.4	38.5	2076	2	AAQ83531	Aaq83531 Sequence
43	673	37.1	2252	2	AAT28022	Aat28022 Chick BMP
44	673	37.1	2252	2	AAV71973	Aav71973 Mouse BMP
45	671.4	37.0	2252	2	AAT27229	Aat27229 Bone morp

Title: US-10-600-645-1  
 Perfect score: 1813  
 Sequence: 1 CTAGTGGATCCCCCGGGCTG.....TTCAGGACTCTGCAGAATGC 1813

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Issued\_Patents\_NA:\*  
 1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*  
 2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*  
 3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*  
 4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*  
 5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*  
 6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1813	100.0	1813	3	US-08-123-934A-1	Sequence 1, Appli
2	1813	100.0	1813	4	US-09-874-628-1	Sequence 1, Appli
3	1813	100.0	1813	5	PCT-US94-10080-1	Sequence 1, Appli
4	1581.4	87.2	2070	3	US-09-382-256-13	Sequence 13, Appl
5	1581.4	87.2	2070	3	US-09-395-115-13	Sequence 13, Appl
6	1581.4	87.2	2070	3	US-08-436-265-13	Sequence 13, Appl
7	1581.4	87.2	2070	3	US-09-679-187-13	Sequence 13, Appl
8	1581.4	87.2	2070	4	US-09-267-963D-13	Sequence 13, Appl
9	1574.2	86.8	2402	3	US-08-462-467B-11	Sequence 11, Appl
10	1574.2	86.8	2402	3	US-08-158-735A-3	Sequence 3, Appli
11	1574.2	86.8	2402	3	US-08-334-179A-11	Sequence 11, Appl
12	1424.4	78.6	2056	3	US-08-158-735A-1	Sequence 1, Appli
13	1387	76.5	2932	2	US-08-481-337A-5	Sequence 5, Appli
14	1387	76.5	2932	3	US-09-382-256-5	Sequence 5, Appli
15	1387	76.5	2932	3	US-09-395-115-5	Sequence 5, Appli
16	1387	76.5	2932	3	US-08-436-265-5	Sequence 5, Appli
17	1387	76.5	2932	3	US-09-679-187-5	Sequence 5, Appli
18	1387	76.5	2932	4	US-08-448-371A-5	Sequence 5, Appli
19	1387	76.5	2932	4	US-09-267-963D-5	Sequence 5, Appli
20	1387	76.5	2932	5	PCT-US95-05467-5	Sequence 5, Appli
21	716	39.5	1952	2	US-08-481-337A-7	Sequence 7, Appli
22	716	39.5	1952	3	US-09-382-256-17	Sequence 17, Appl

23	716	39.5	1952	3	US-09-395-115-17	Sequence 17, Appl
24	716	39.5	1952	3	US-08-436-265-17	Sequence 17, Appl
25	716	39.5	1952	3	US-09-679-187-17	Sequence 17, Appl
26	716	39.5	1952	4	US-08-448-371A-7	Sequence 7, Appli
27	716	39.5	1952	4	US-09-267-963D-17	Sequence 17, Appl
28	716	39.5	1952	5	PCT-US95-05467-7	Sequence 7, Appli
29	697.4	38.5	2076	3	US-08-123-934A-3	Sequence 3, Appli
30	697.4	38.5	2076	4	US-09-874-628-3	Sequence 3, Appli
31	697.4	38.5	2076	5	PCT-US94-10080-3	Sequence 3, Appli
32	673	37.1	2252	3	US-08-462-467B-13	Sequence 13, Appl
33	673	37.1	2252	3	US-08-334-179A-13	Sequence 13, Appl
34	647	35.7	706	3	US-08-462-467B-19	Sequence 19, Appl
35	440.8	24.3	469	3	US-08-462-467B-15	Sequence 15, Appl
36	438.8	24.2	466	3	US-08-158-735A-5	Sequence 5, Appli
37	405	22.3	1647	3	US-08-123-934A-7	Sequence 7, Appli
38	405	22.3	1647	4	US-09-874-628-7	Sequence 7, Appli
39	405	22.3	1647	5	PCT-US94-10080-7	Sequence 7, Appli
40	403.4	22.3	2333	3	US-09-382-256-7	Sequence 7, Appli
41	403.4	22.3	2333	3	US-09-395-115-7	Sequence 7, Appli
42	403.4	22.3	2333	3	US-08-436-265-7	Sequence 7, Appli
43	403.4	22.3	2333	3	US-09-679-187-7	Sequence 7, Appli
44	403.4	22.3	2333	4	US-09-267-963D-7	Sequence 7, Appli
45	401.8	22.2	2160	3	US-09-382-256-15	Sequence 15, Appl

Title: US-10-600-645-1  
 Perfect score: 1813  
 Sequence: 1 CTAGTGGATCCCCCGGGCTG.....TTCAGGACTCTGCAGAATGC 1813

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : EST:\*  
 1: gb\_est1:\*  
 2: gb\_est2:\*  
 3: gb\_htc:\*  
 4: gb\_est3:\*  
 5: gb\_est4:\*  
 6: gb\_est5:\*  
 7: gb\_est6:\*  
 8: gb\_gss1:\*  
 9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	% Query		Length	DB	ID	Description
	Score	Match				
1	1389.6	76.6	1521	9	AY411158	AY411158 Mus muscu
2	1274.6	70.3	1532	9	AY411156	AY411156 Homo sapi
3	1002.2	55.3	1532	9	AY411157	AY411157 Pan trogl
4	774.6	42.7	1121	4	BM473726	BM473726 AGENCOURT
5	736	40.6	874	1	AU124197	AU124197 AU124197
6	717.2	39.6	1911	3	AK086130	AK086130 Mus muscu
7	715.6	39.5	779	7	CK638737	CK638737 UI-M-HO0-
8	710	39.2	1509	9	AY418115	AY418115 Mus muscu
9	707.6	39.0	783	7	CF744610	CF744610 UI-M-GV0-
10	702	38.7	1509	9	AY418113	AY418113 Homo sapi
11	682.6	37.7	769	6	CD351417	CD351417 UI-M-GI0-
12	672.8	37.1	1509	9	AY418114	AY418114 Pan trogl
13	668.4	36.9	909	5	BU152346	BU152346 AGENCOURT
14	667.2	36.8	804	7	CN530503	CN530503 UI-M-HO0-
15	666.6	36.8	772	7	CN460181	CN460181 UI-M-HB0-
16	664.8	36.7	717	7	CO045435	CO045435 UI-M-HO0-
17	664.8	36.7	775	6	CD352514	CD352514 UI-M-GI0-
18	662.2	36.5	807	1	AU124052	AU124052 AU124052
19	652	36.0	708	7	CN457827	CN457827 UI-M-HN0-



20	651.2	35.9	736	6	CA749455
21	639	35.2	722	7	CF534538
22	635.8	35.1	689	7	CN535314
23	629.2	34.7	1073	7	CN643937
24	625.6	34.5	741	7	CF741390
25	621.6	34.3	849	6	CD244444
26	618.4	34.1	750	6	CD804808
27	616.8	34.0	817	6	CD352073
28	608.6	33.6	698	7	CN533447
29	602.4	33.2	978	4	BI767168
30	598.4	33.0	632	7	CK626617
31	593	32.7	625	7	CN664087
32	590	32.5	773	1	AU123612
33	588.2	32.4	995	7	CN646618
34	583.4	32.2	653	6	BY732642
35	560.2	30.9	613	7	CN670354
36	556.4	30.7	621	1	AA137882
37	544.2	30.0	679	7	CK965863
38	537.2	29.6	702	7	CN534002
39	536.4	29.6	757	7	CO424454
40	535.8	29.6	616	4	BI684168
41	535.2	29.5	649	2	BE282214
42	518.4	28.6	626	6	CB045957
43	515.8	28.5	559	7	CN668685
44	513.8	28.3	557	6	CA566919
45	508	28.0	627	7	CN683840

CA749455	UI-M-FY0-
CF534538	UI-M-GI0-
CN535314	UI-M-HS0-
CN643937	ILLUMIGEN
CF741390	UI-M-GH0-
CD244444	AGENCOURT
CD804808	UI-M-GW0-
CD352073	UI-M-GI0-
CN533447	UI-M-HO0-
BI767168	603060542
CK626617	mj24b01.y
CN664087	A0808E07-
AU123612	AU123612
CN646618	ILLUMIGEN
BY732642	BY732642
CN670354	A0891G12-
AA137882	mq80a04.r
CK965863	4080965 B
CN534002	UI-M-HO0-
CO424454	UI-M-HU0-
BI684168	603306579
BE282214	601100839
CB045957	NISC_gf01
CN668685	A0870E02-
CA566919	K0407E10-
CN683840	E0184B12-